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GAP of: X69922.gb_pl check: 4491 from: 1 to: 1423

JOCUS
DEFINITION      P. sylvesteris mRNA for glutamine synthetase.
ACCESSION       X69922
VERSION         X69822.1
KEYWORDS        gin gene, glutamate-ammonia ligase; glutamine synthetase.
SOURCE          Pinus sylvesteris (scots pine)
ORIGIN          1
...
GAP of: X69922.gb_pl check: 9167 from: 1 to: 1434

JOCUS
DEFINITION      Pisum sativum glutamine synthetase (cytosolic GS1) mRNA, complete
ACCESSION       X69837
VERSION         M20663.1
KEYWORDS        Glutamine synthetase (cytosolic GS1) . . .
SOURCE          M20663.1
ORIGIN          1
...
Symbol comparison table: /$TSD/app/igsi/gscore/data/rundata/musgpadm.cmp
ComCheck: 8760

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Gap Weight:      1      Average Match: 10.000
Length Weight:   0      Average Mismatch: 0.000

Quality: 10444      Length: 1571
Ratio: 7.339        Gaps: 166
Percent Similarity: 82.504      Percent Identity: 82.504

Match display thresholds for the alignment (s):
      = 1
      = 5
      = 10

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x69822.gb pl x m20663.gb pl November 25, 2003 14:18

1 ...T...TC.....C...CTTCC.....TC.....TGGTGGTGGT...22
21 CGCTGATCTGAGAGTCTATCATCCACACAGCTGATCAATTT...50
23 CAGGAGAGGCG.....CAGGTCGAGCGGTGTT...AA...CAG...CTC...56
31 ...CA...AGTTCTTTTTC...T...TC...A...CTTTTCAAACAGCTCTCTTTCA...94
37TC...TGC...CTGAC...C...CTGAGCT...ACGTGACACAGAGGTGATTC...98
45 GATCTCATCAAGCTGATGTTCTGAG...GAGC...CAGCGAAGAAATGCTG...141
49 AGATATATATGATATGAGTACAGATGAC...TATTCGACAT...AAG...145
102 AGATATATATGATATGAGTACAGATGAC...TATTCGAGT...TGG...148
112 AGATATATGATATGAGTACAGATGAC...TATTCGAGT...TGG...158
146 CCA...GATCTCTGT...CAGGACGTGTGAT...AGGCTTAAGAGCTGTCCAA...192
159 CAGGA...CTCT...TCCGAGACAGCTCTGATACCTT...CAGAGTCTCCGAG...235
193 TGGACATGACGCGTCCAGCTACGACAGGAGGTCTAAGGACATGAGACGCA...242
233 TGGATATATGATGTTCCGACGAGGACAGCTCTGCTGACAGTATGTA...285
246 ATGTGCT...TCATGTCACAGCTA...TCTCTGCTGCTGCTGCT...GGAGG...289
286 AGTTATCT...TATACCAACAGCCTTTTTAAG...GATCCA...TTGACAGAGG...325
290 GAGAGGAT...T...TGGTATCTGTGATCTATCTCTCAATGG...G...AC...335
333 GTAA...C...CATCTGCTGTATGTGTGATGCTGATCTGCTGAGAGC...380
336 TGTATTTCTTTC...C...ACAGAGGCGC...TGCAGAGGAGAAATTTTTTAAG...426
381 ...CAATTC...GCTACCA...AGAGCCAGCTGCTGAGCTGT...G...434
383 AAAGAGG...G...GTGAG...TCATGAGAGGATCTGATAGGCTT...T...GACGA...436

[illegible]

1249 G...GACATG GCTTGGTGT...TCTTG.T.TANGG.T.TCA 1279
1289 TATATATTITTTATTT.TGTCTACTTG...TA.ATAG.G.CAGGGCT 1331
1290 CAGCT.TGTATTT.TCT.TTC...CTGTCTACTTAGGTC.A...C. 1320
1332 TTA.AGAGCTCTTT..TTAC...T.T..TATATTCGGTG.TGAA 1372
1321 ..AATATATCTATGGCTTATCTAGTATATATTT...GTCTATG.T 1365
1373 GATGATT.GACAAAT..TG..TTAGATG...T..T..TGATAT 1408
1366 GAT.TATATATATATGATATGATATGATATGCCAGTATATGAT 1414
1409 GATAT.A...T.TCTTTCT.G 1423
1415 GATAGAGGCTCTCTTTG 1434